

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 30, 2002, 17:44:56 ; Search time 115.69 seconds
(without alignments)
1235.267 Million cell updates/sec

Title: US-09-357-273a-2
Perfect score: 5139
Sequence: 1 MPARLLLLTLPLGLGIF.....QPYFHPPEPPQPVTPDAL 977

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhcc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5139	100.0	977	4	075460
2	4741	97.7	977	11	09EOYO
3	2192.5	42.7	911	11	0922E3
4	2017	39.2	408	11	09D340
5	1604.5	31.2	1038	5	09VDT7
6	959.5	18.7	1072	3	094537
7	770	15.0	893	10	09FS17
8	755.5	14.7	939	10	09FRM6
9	727	14.1	841	10	09C5S2
10	655.5	12.8	393	10	09SHL6
11	529.5	10.3	354	10	09SFI2
12	416	8.1	169	1	09C4S9
13	334	6.5	1114	11	0922B5
14	320	6.2	1230	3	09HFT9
15	312	6.1	1108	11	0921Z1
16	309	6.0	666	3	042625
17	306	6.0	735	11	09ERU7
18	299.5	5.8	536	3	09P466
19	297.5	5.8	1077	5	019192

20	295	5.7	1257	10	064768
21	293.5	5.7	360	5	094608
22	290	5.6	527	13	09PW62
23	290	5.6	793	3	09HFW2
24	286.5	5.6	360	5	094609
25	286	5.6	842	10	09FNU3
26	285	5.5	311	5	096526
27	285	5.5	525	13	057318
28	283.5	5.5	530	3	042793
29	283.5	5.5	823	3	09HFR3
30	283.5	5.5	1152	5	017346
31	283	5.5	311	5	015851
32	283	5.5	350	5	09NG91
33	283	5.5	482	5	09U600
34	283	5.5	518	5	09NH57
35	283	5.5	520	5	09NH60
36	282	5.5	302	5	09NH56
37	282	5.5	302	5	09NH55
38	282	5.5	533	5	09NH59
39	282	5.5	571	5	09NH58
40	281	5.5	547	5	021431
41	280.5	5.5	1271	10	09LX30
42	279	5.4	493	5	09V495
43	279	5.4	825	10	09AKL7
44	279	5.4	1054	10	09EKL3
45	279	5.4	1096	5	017368

ALIGNMENTS

RESULT 1
ID 075460
AC 075460
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE PROTEIN KINASE/ENDORIBONUCLEASE.
GN IREL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RX MEDLINE=98301437; Pubmed=9637683;
RA Tirasophon W., Welihinda A.A., Kaufman R.J.;
RT "A stress response pathway from the endoplasmic reticulum to the
RT nucleus requires a novel bifunctional protein kinase/endoribonuclease
RT (irelp) in mammalian cells."
RL Genes Dev. 12:1812-1824 (1998).
CC EMBL: AF059198; AAC25991.1;
DR InterPro: IPR002372; Bac_P00_repeat.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR001005; Myb_DNA_bind.
DR Pfam: PF01011; Bacterial_P00; 2.
DR InterPro: IPR002290; Ser_Thr_kin_actsite.
DR Pfam: PF00069; Pkinase; 1.
DR PROSITE: PS00037; MYB_1; UNKNOWN_1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-Binding; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 977 AA; 109686 MW; EAFSEI082D09010C CRC64;

Query Match 100.0%; Score 5139; DB 4; Length 977;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPARLLLLTLPLGLGIFGSTVTLPEFLFVSTLDGSLHAVSKRTGSIKWTLEKDP 60

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|||||
Db 1 MPARLLLLLLLLLPGLCIFGTSSTVTLPELTLFVSTLDGSLHAASKRTGSIKMTLKEDP 60
QY 61 VLOVPTHEEPAPLPDPNDGSLYTLGSKNNNGELTPELTPELVQASCRSSDGLTYMGK 120
Db 61 VLOVPTHEEPAPLPDPNDGSLYTLGSKNNNGELTPELTPELVQASCRSSDGLTYMGK 120
QY 121 KODIIVYIDLTLGKQOQLSSAFADSLCPSTSLYLGRTVEYITMYDPKTRELRNATYF 180
Db 121 KODIIVYIDLTLGKQOQLSSAFADSLCPSTSLYLGRTVEYITMYDPKTRELRNATYF 180
QY 181 DYASLPDEBDYKMSHFVNSGDCLVTVVDSGCVLIQNTASPVAFYVQREGKLV 240
Db 181 DYASLPDEBDYKMSHFVNSGDCLVTVVDSGCVLIQNTASPVAFYVQREGKLV 240
QY 241 MHINAVETLRYLPFMSGEVGRITKMKYPRPKETBAKSKLPVTVGAYSTSLYASPSMV 300
Db 241 MHINAVETLRYLPFMSGEVGRITKMKYPRPKETBAKSKLPVTVGAYSTSLYASPSMV 300
QY 301 HEGVAVVPRGSTLPLEGGPQTDGVTIGDKGECVITPSTVKNFDPGLKSKNKLNYLRNYL 360
Db 301 HEGVAVVPRGSTLPLEGGPQTDGVTIGDKGECVITPSTVKNFDPGLKSKNKLNYLRNYL 360
QY 361 LIGHHTPLASTKMLEFPNNLPKHNENVPADSEKSFEEVITLVQTSNATYTSR 420
Db 361 LIGHHTPLASTKMLEFPNNLPKHNENVPADSEKSFEEVITLVQTSNATYTSR 420
QY 421 DVEEKPAHAPRPAVPSMLKDMATILSTFLIGWAFITTYPLSMHQOOLQHOQF 480
Db 421 DVEEKPAHAPRPAVPSMLKDMATILSTFLIGWAFITTYPLSMHQOOLQHOQF 480
QY 481 KELEKIQLLQOQOOLPFPHPGDTAODGELDTSGPYSESSGTSPTSPPRASNSHLSG 540
Db 481 KELEKIQLLQOQOOLPFPHPGDTAODGELDTSGPYSESSGTSPTSPPRASNSHLSG 540
QY 541 SSASAGSSPSEDDDGDETSVYVKGISFCPKVYLGHGAGTIVYGMEDNRYAVAKR 600
Db 541 SSASAGSSPSEDDDGDETSVYVKGISFCPKVYLGHGAGTIVYGMEDNRYAVAKR 600
QY 601 ILPECFSPADREVOQLRSDENPNVIRYFCTEKDRQFOYIAELCAATLOEYVEQKFAH 660
Db 601 ILPECFSPADREVOQLRSDENPNVIRYFCTEKDRQFOYIAELCAATLOEYVEQKFAH 660
QY 661 LGLEPITLQOQTSGLAHSLNIVHDLKPHNLIISMPNAGKIKAMISDFGLCKILAV 720
Db 661 LGLEPITLQOQTSGLAHSLNIVHDLKPHNLIISMPNAGKIKAMISDFGLCKILAV 720
QY 721 GRHSRSRSGVGTGEGTAPRMLSDCKENPTYVDIFSACGVFYVVSSESHPRGSKLQ 780
Db 721 GRHSRSRSGVGTGEGTAPRMLSDCKENPTYVDIFSACGVFYVVSSESHPRGSKLQ 780
QY 781 RQANILLGACSLDCLHPEKHEDVIARELIEKMIAMDPOKRSANDVILKHPFWSLEKOLQ 840
Db 781 RQANILLGACSLDCLHPEKHEDVIARELIEKMIAMDPOKRSANDVILKHPFWSLEKOLQ 840
QY 841 FFQOVSDRIEKESLDGPIVQOLERGRAVVKMDRENITDPLQTDLRKFRYKGGSVBDL 900
Db 841 FFQOVSDRIEKESLDGPIVQOLERGRAVVKMDRENITDPLQTDLRKFRYKGGSVBDL 900
QY 901 LRAHRNKNHNRBELPAVEKRETLGLTPDQFVGYTSRPHLANTYRAMELCSHERLPQY 960
Db 901 LRAHRNKNHNRBELPAVEKRETLGLTPDQFVGYTSRPHLANTYRAMELCSHERLPQY 960
QY 961 YFHERPERQPVTPDAL 977
Db 961 YFHERPERQPVTPDAL 977
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DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, last annotation update)
Db PROTEIN KINASE/ENDORIBONUCLEASE(IRE1) ALPHA.
GN IRE1A OR IRE1 ALPHA
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11446108;
RA Miyoshi K., Katsuyama T., Imaizumi K., Taniguchi M., Mori Y.,
RA Hitomi J., Yui D., Manabe T., Gomi F., Yoneda T., Tohyama M.;
RT "Characterization of mouse Irelalpha: cloning, mRNA localization in
RT the brain and functional analysis in a neural cell line.";
RL Mol. Brain Res. 85:68-76(2000).
DR EMBL, AB031332; BAB20901.1; -.
DR MGD; MGI:1930134; Irela.
DR InterPro: IPR002372; Bac_PQO_repeat.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR InterPro: IPR001245; Tyr_kin.
DR Pfam; PF01011; Bacterial_PQO; 2.
DR Pfam; PF00063; Pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Kinase; Transferase.
SQ SEQUENCE 977 AA; 110184 MW; 216E3E2PA2FF370 CRC64;

Query Match 92.3%; Score 4741; DB 11; Length 977;
Best Local Similarity 92.2%; Pred. No. 0;
Matches 903; Conservative 34; Mismatches 38; Indels 4; Gaps 2;

QY 1 MPARLLLLLLLLL--PGLIFGTSSTVTLPELTLFVSTLDGSLHAASKRTGSIKMTLK 58
Db 1 MPARLLLLLLLLLPPPGSFGRTSTVTLPELTFLFVSTLDGSLHAASKRTGSIKMTLK 60
QY 59 DPLVQPTHEEPAPLPDPNDGSLYTLGSKNNNGELTPELTPELVQASCRSSDGLTYMG 118
Db 61 DPLVQPTHEEPAPLPDPNDGSLYTLGSKNNNGELTPELTPELVQASCRSSDGLTYMG 120
QY 119 GKQODIIVYIDLTLGKQOQLSSAFADSLCPSTSLYLGRTVEYITMYDPKTRELRNAT 178
Db 121 GKQODIIVYIDLTLGKQOQLSSAFADSLCPSTSLYLGRTVEYITMYDPKTRELRNAT 180
QY 179 YEDVYASLPDEBDYKMSHFVNSGDCLVTVVDSGCVLIQNTASPVAFYVQREGKLV 238
Db 181 YEDVYASLPDEBDYKMSHFVNSGDCLVTVVDSGCVLIQNTASPVAFYVQREGKLV 240
QY 239 KVMHINAVETLRYLPFMSGEVGRITKMKYPRPKETBAKSKLPVTVGAYSTSLYASPS 298
Db 241 KVMHINAVETLRYLPFMSGEVGRITKMKYPRPKETBAKSKLPVTVGAYSTSLYASPS 300
QY 299 MVHEGVAVPRGSTLPLEGGPQTDGVTIGDKGECVITPSTVKNFDPGLKSKNKLNYLRNY 358
Db 301 MVHEGVAVPRGSTLPLEGGPQTDGVTIGDKGECVITPSTVKNFDPGLKSKNKLNYLRNY 360
QY 359 WLLIGHHTPLASTKMLEFPNNLPKHNENVPADSEKSFEEVITLVQTSNATYTSR 418
Db 361 WLLIGHHTPLASTKMLEFPNNLPKHNENVPADSEKSFEEVITLVQTSNATYTSR 420
QY 419 SRDVEEKPAHAPRPAVPSMLKDMATILSTFLIGWAFITTYPLSMHQOOLQHOQ 478
Db 421 SRDVEEKPAHAPRPAVPSMLKDMATILSTFLIGWAFITTYPLSMHQOOLQHOQ 480
QY 479 FQKLEKIQLLQOQOOLPFPHPGDTAODGELDTSGPYSESSGTSPTSPPRASNSHLS 538
Db 481 FQKLEKIQLL--QOQOOLPFPHPGDTAODGELDTSGPYSESSGTSPTSPPRASNSHLS 538
QY 539 SGSSASAGSSPSEDDDGDETSVYVKGISFCPKVYLGHGAGTIVYGMEDNRYAV 598
Db 541 SGSSASAGSSPSEDDDGDETSVYVKGISFCPKVYLGHGAGTIVYGMEDNRYAV 600
```

Db 539 PSSASRAGTSPSLSEODEDEETRMVIVGKISPCRDVLGHGAGETIYVKGFMNDNVAV 598
QY 599 KRILPECSFADREVQLRESDEHPNVIYRFTCEKROFOYIAIELCATLOEYEQKF 658
Db 599 KRILPECSFADREVQLRESDEHPNVIYRFTCEKROFOYIAIELCATLOEYEQKF 658
QY 659 AHLGLEPTLLQOTTSGLAHLHSLNIVHRLDKPHNIIILSMPNAGKIKAMISDFGLCKKL 718
Db 659 AHLGLEPTLLQOTTSGLAHLHSLNIVHRLDKPHNIIILSMPNAGKIKAMISDFGLCKKL 718
QY 719 AVGRHSFRSRRGSGVPTGEWIAPEMLSEDCKNPTTYVDIFSAGCYFYVVSQSPFGKS 778
Db 719 AVGRHSFRSRRGSGVPTGEWIAPEMLSEDCKNPTTYVDIFSAGCYFYVVSQSPFGKS 778
QY 779 LORQANILGACSLDCLPEKHEDVIARELLEKMIAMPORPSANDVLKHPFFSLERQ 838
Db 779 LORQANILGACSLDCLPEKHEDVIARELLEKMIAMPORPSANDVLKHPFFSLERQ 838
QY 839 LOFQDVSDRIEKESLDSPIVKOLERGGRAVVKMDRENITDPLQDLRKFRYKGSVR 898
Db 839 LOFQDVSDRIEKESLDSPIVKOLERGGRAVVKMDRENITDPLQDLRKFRYKGSVR 898
QY 899 DLIRAMRKHHYRLPVEVRETGLTLPDDYVCYTSRPHILATYRAMELCSHERLFQ 958
Db 899 DLIRAMRKHHYRLPVEVRETGLTLPDDYVCYTSRPHILATYRAMELCSHERLFQ 958
QY 959 PYFHEPEPOPVPYPPAL 977
Db 959 PYFHEPEPOPVPYPPAL 977
RESULT 3
0922E3 PRELIMINARY: PRT: 911 AA.
AC 0922E3
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE IREL.
GN IREL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=98429494; PubMed=9755171;
Wang X.Z., Harding H.P., Zhang Y., Jolicœur E.M., Kuroda M., Ron D.;
"Cloning of mammalian Irel reveals diversity in the ER stress
responses.";
EMBO J. 17:5708-5717(1998).
CC -I- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF071777; AAC64400.1; -.
DR MGD: MGI:1349436; Irel.
DR InterPro: IPR002372; Bac_PQO_repeat.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF01011; Bacterial_PQO; 1.
DR Pfam: PF00069; pkinase; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; transferase.
SEQUENCE 911 AA; 101355 MW; 173EDEL63841FE7 CRC64;

Query Match 42.7%; Score 2192.5; DB 11; Length 911;
Best Local Similarity 47.7%; Pred. No. 2.8e-159;
Matches 478; Conservative 123; Mismatches 267; Indels 135; Gaps 20;

QY 2 PARRLILLTLLPLGLFGSTVTLPEPTLFFVSTLDSGLAVSKRSGISIKWTLEKDDV 61
Db 13 PLGLILLQVTL---LGLKLPQVQSVRPESLTFVSTWDSGLHALNKQTDLKWTKVDDPI 68

QY 62 LQVPHVEEPAFLPDPNDGSLVTLGSKNNEGTLKLPETIPELVQASPCRRSDGILYMKK 121
Db 69 IGGPMYVTEMAFLSPADGSLVTLGTHKLGKMLPFTIPELVHASPCRRSDGVEYTGK 128
QY 122 QDIWIVIDLITGEKQOOTSANFADSLCSTSLIYLGRFEYITIMDTRELRNATYFD 181
Db 129 QDWFVVPDESGETMTLT---EGL--STPQLFGRQYVSMHDLRTPALRMNTYR 183
QY 182 YAASLPDEGDYKMGHFNPSNGDVLVTVDESQDVLMTIONVSPAVAFVMOREGLRKM 241
Db 184 YSAPILNSPGKYMHLNLSGKGLITVDPGSGIYLMTODLGVPYTGITYHNDLHQLP 243
QY 242 HINVAETLRVLTFSNGEVRITKWKYPPEKTEAK---SKLPITYVGRYSTLYAS 296
Db 244 HLTLRDLTLHFLVRMGTI-RLPASSY---QPTAFQSSLDLQMLTLYVGRKEEAGFYVS 299
QY 297 PSMVEGVAANVRGSLTPLLSEGPOTDGTIGKGEVITPSTVDKFPDGLKKNLNTLR 356
Db 300 KALVAGVALVVRGLTLPMDGPTIDEVTLQVSGERESPSTAVRPSGSAV-----LP 353
QY 357 NYWLLIGHETPLASTKMLERFPNNLPKRENVIPADESKS-----FEEVINYDQ 409
Db 354 SQMLLIGHETPPVYLHTMLRVHP--IP---GKVSATRASDELHAPVFEELLNRE 407
QY 410 TSENAPTVSRDVEKPAHAPAPAPVDSM---LKDMATILSTELLIGVAFITYP 465
Db 408 DEPLRP-----EEKAS-----DSYGLGSQDLAATFPAILLGAVALY----- 445
QY 466 LSMHQQOOLQHOQFOKELEKIOLOOQOQOLPFPH--PEDTAQDC-----ELDTSGPY 517
Db 446 -----LMROOQSPSAPAGPDLQDAQOLSRDILDORRF 482
QY 518 SESSGTSPTSPPRASNHSLSGSSAKASSPSLEQDDGDETSVYIKISPCPKVL 577
Db 483 QSPSEPAQPHDPEAGQPT-----VVGKISFNPKVL 514
QY 578 GHGAGETIYRGMPFNRDVAVKRIILPECSFADREVQLRESDEHPNVIYRFTCEKROF 637
Db 515 GRAGGTIVFRGQFEGRAVAVKRLRREGCVLRREVQLQESDRHPNVIYRFTCEHGRQF 574
QY 638 QYIAIELCATLOEYEQKDFAHGLLEPTLLQOTTSGLAHLHSLNIVHRLDKPHNIIIS 697
Db 575 HYIALELCQASLOEYVESDLDRCGLEPTTVLQOMMSGLAHLHSLNIVHRLDKPHNIIIA 634
QY 698 MPNAGKIKAMISDFGLCKKLAVGRHSFRSRRGSGVPTGEWIAPEMLSEDCCKENPTTYVD 757
Db 635 GPDSSQGGKVVVLSDFGLCKKLFPVGRCSFSLHSGIPETBSMMAPELLOLP-PDPTNAVYDI 693
QY 758 FSAGCVFYVVSSESHPEKSLQROANILGACSLDCLPEKHEDVIARELLEKMIAMP 817
Db 694 FSAGCVFYVVSSESHPEKSLQROANILGACSLDCLPEKHEDVIARELLEKMIAMP 817
QY 818 QKRPASANDVLKHPFFWSLEKQLQFQDVSDRIEKESLDSPIVKOLERGGRAVVKMDREN 877
Db 754 QDRPSAGWLAPHLFWSRAKELQFQDVSDWLEKBPDOGRPLVSALAEAGSYKVVREDMNRH 813
QY 878 TNDPLQDLRKFRYKGSVRDLIRAMRKHHYRLPVEVRETGLTLPDDYVCYTSR 937
Db 814 ISAPLQADLKRRTYKGSVRSQDLIRAMRKHHYRLPVEVRETGLTLPDDYVCYTSR 937
QY 938 PHLAHTYRAMELCSHERLFQPYFHEPEPOPVPY---TPDA 976
Db 874 PRLLLHTHRAMRTCASSESLFLPY-----PPLAERPRDA 908

RESULT 4
Q9D340 PRELIMINARY: PRT: 408 AA.
AC Q9D340;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE 903041AB18RIK PROTEIN.

Query Match	Similarity	95.8%	Score	2017:	DB	11:	Length	408:
Best Local	Similarity	95.8%	Pred	No	2.2e-146:			
Matches	388:	Conservative	5:	Mismatches	10:	Indels	2:	Gaps
QY	1	MPARLLLLLLLL--PGLGIFGSGTSTVTLPETLFVSTLDGSLHAVSKRTGSIKWTLKE	58					
Db	1	MPARWLLLLLLLLPPPGSGSGRTSTVTLPETLFVSTLDGSLHAVSKRTGSIKWTLKE	60					
QY	59	DPVLVPVTHVEBPALPDNDGSLVTGICKNNEGLTKLPETLPETLVOASPCSSDGLM	118					
Db	61	DPVLVPVTHVEBPALPDNDGSLVTGICKNNEGLTKLPETLPETLVOASPCSSDGLM	120					
QY	119	GKKODIWIYIDLTEGEKOOTLSAFADSLCPSTSLYLGRTEYTIYMDTKRELKMNAT	178					
Db	121	GKKODIWIYIDLTEGEKOOTLSAFADSLCPSTSLYLGRTEYTIYMDTKRELKMNAT	180					
QY	179	YEDVAASLPDEGDGXKMSHFVNSNGGGLVTVYSESGDVLMIQNVASPVAAVFMQREGR	238					
Db	181	YEDVAASLPDEDDVDYKMSHFVNSNGGLVTVYSESGDVLMIQNVASPVAAVFMQGEVLR	240					
QY	239	KVMHINVAEVLRLYLFMSGEGVRLTKMKYPPPKETEAASKLPTLYLGVKYSTSLASPS	298					
Db	241	KVMHINVAEVLRLYLFMSGEGVRLTKMKYPPPKETEAASKLPTLYLGVKYSTSLASPS	300					
QY	299	MVHEVAVAVPRGSTLPRLLEGPGTODGVITGDKKECVITPSTDYKFPDGLSKMKNLRLNY	358					
Db	301	MVHEVAVAVPRGSTLPRLLEGPGTODGVITGDKKECVITPSTDYKFPDGLSKMKNLRLNY	360					
QY	359	WLLIGHNETPLSASTKMLERFPNNLPKIHRENIIPADSEKKSFEVY	403					
Db	361	WLLIGHNETPLSASTKMLERFPNNLPKIHRENIIPADSEKKSFEVY	405					
RESULT	5							
99VDP7								

Query Match	31.2%	Score 1604.5;	DB: 5;	Length 1038;
Best Local Similarity	37.5%	Pred. No. 4.6e-114;		
Matches 379;	Conservative 152;	Mismatches 276;	Indels 203;	Gaps 31.

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Db 27 NVQVPHPLPDRDGSITYOLGQMS--LKKLPYIPOLVANAPCRSSDGILYSGKSDTWY 84
OY 127 VIDLTGKQOQLSSAFADSLC-----PSTSLYLGRTEVTITMYDF--KTRELR 174
Db 85 MYDPYTGKREKVM--GFGDQVYDKEGEQIGWATSRATYLGTYQVYMYDLSLANKKADK 142
OY 175 -WNAIYFYAA--SLPEDEGDYKMSHFVNSGDLVYTVDSGDIYMIQNYASPVYAFVY 231
Db 143 PNIITFYDYNASAPPELAKKEYEYIHLITTTNGQIVTIDRKIKGKFLMODLSSPVYAAFL 202
OY 222 WOREGLRKVMHINAVETLRVLTMS--GEVGRITKMKYPPKPEAKSKLPTLYVGY 289
Db 203 LGPDDLSPPTTVDQVDEVAQALLESKGTGNVNTV-----KLFQSLYVGEH 247
OY 290 SNTLSAASQWMEGVAVYVPGSTLP--LLBGPQDGVYIGDKGECVITPSPDYKFPDL 346
Db 248 QKGLALPSLVAKN--TPRISTAPPIKLDGP-----TGQNSNOEDPRTIYINDVL 298
OY 347 KSKNKLNTLRNWLIGHNE-----TPLSASTKMLRFRPNLPRKHEN--VIP 392
Db 299 Q-----EHAGIMIGHNMNPNEGNGNLQSLPTASSKVVQSLAT--IHNYNDGYGLL 347
OY 303 ADSEKKSFE-----EYVNL-VDO-----TSENAPTVSRDVEEKPAHA---PARPA 435
Db 348 ANNEKNADIGVQDPELVEIGIDQRTNGNTINRTKITILQNSNKVQAFINEMFMEHPSG 407
OY 436 PYDSMLAKMATIITLSTFLLIGVAVITPYPLSMHQQOQLHQOFOKELEKIQLLQOQOQ 495
Db 408 KWHQIL-----IYVLGMIA-LFWYTCST-----MKELOK----- 436
OY 496 LPHFPGDQADGELLDTSGPYSESSGTSPTSPRASNSHLSGSSAKAGSPSELOD 555
Db 437 -----QSENGSKTFALQNGSNGS--TGSNGSNANAEDLVLDG 472
OY 556 DQDEETSVYVIGKISFCPKDVLGHAEGTIVYRGMFNDQVAVKRIILPCFSFADREVOL 615
Db 473 NQO-----VRGKISFSTNEVLGKCEGTFEVEEFVAKRLLPCEFTFADREVAL 527
OY 616 LRESDEHVRVIFCTEKKOROFQYALTELCATLOEYVQKQFAHL--GLEPITLLOQT 673
Db 528 LRESDAHEWVYKFTEDQRFRTAVELCAATLQDYTEGDRSLELQNHIDWQVLSQAA 587
OY 674 SGLAHLHSINIYVHDLKPHNIIISMPNAGKIKAMISDFGLCKLAVGRHSFSRSGVPG 733
Db 588 SGLSHLSLDIYHDIKPNQNLISLPDAKGVYVMSDFGLCKLNFKGTFSRSRSGVPG 647
OY 734 TEGVLAPEML-----SEDCKENPTY-----TVDFISAGCYFTYV 767
Db 648 TDGWLAPPEMRSQRTVRHDFYUYPULLLHNHKNFLKMSFNYLQTTAVDIFISGCVYVVY 707
OY 768 VEGSHPEGKSLQROANITLGCASLDCLEPEKHED--VIARELLEKMIADPOKRPQA 823
Db 708 LSGHHHAGDNLKROANILISHEYNLAKLRPEDDSEDSRIILAEQLSDMIHKOPORRPA 767
OY 824 NDVLKHPFMSLEKOLQFQDVSDRIEKESLDGPYVQLERGRAVVKMDMRENTIDPQL 883
Db 768 RIGIHNPLFWDPRKMLSFQDVSDREKQGFHAERPLKSEKNGRIYVLDWMVHIDPMIT 827
OY 884 TDLKRFRTYKGGSVRDLLRAMRNKKHNYRELAEVARETIGTLPDQFVCTYSRFPYLLAH 943
Db 828 DDLRYTGRYMGASVVDLRLALRNKKHNYHELTPPAOKMGLCIPHEFTNVAWVRPOLLISH 887
OY 944 TVRAMELCSHERLQPYU-----FHPR-----PEQOPRV 972
Db 888 AYHAHSICSNPEIFKPYISAGYLFTRPMYFDADDALEPMLMDPKPLKI 937

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RESULT 6
O94537 PRELIMINARY: PRT: 1072 AA.
AC O94537:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
BT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

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DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PROBABLE SERINE/THREONINE-PROTEIN KINASE C167.01 PRECURSOR
DE (EC 2.7.1.-).
GN SPAC167.01.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX Schizosaccharomyces.
NX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Rieger M., Wood V., Rajandream M.A., Barrell B.G.;
RL Submitted (Jan-1999) to the EMBL/Genbank/DBS databases.
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ENDOPLASMIC
CC RETICULUM (BY SIMILARITY).
CC - PTM: AUTOPHOSPHORYLATED PRIMARILY ON SERINE RESIDUES (BY
CC SIMILARITY).
DR EMBL: AL035248; CAA22846.1; -.
DR InterPro: IPR002372; Bac_PQO_repeat.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF01011; Bacterial_PQO; 2.
DR Pfam: PF00069; pkinase; 1.
DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; Transmembrane; Signal; Transferase;
KW Serine/threonine-protein kinase; ATP-binding; Glycoprotein;
KW Endoplasmic reticulum; Phosphorylation.
FT SIGNAL 1 30
FT CHAIN 31 1072
FT FT PROBABLE SERINE/THREONINE-PROTEIN KINASE
FT C167.01.
FT DOMAIN 31 518 LUMENAL (POTENTIAL).
FT TRANSMEM 519 539 POTENTIAL.
FT DOMAIN 540 1072 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 29 34 POLY-SER.
FT DOMAIN 654 938 PROTEIN KINASE.
FT NP_BIND 660 668 ATP (BY SIMILARITY).
FT BINDING 682 682 ATP (BY SIMILARITY).
FT ACT_SITE 774 774 BY SIMILARITY.
FT MOD_RES 813 813 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 814 814 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 1072 AA; 121222 MW; 5B1A60EEFC802526 CRC64;

Query Match 18.7%; Score 959.5; DB 3; Length 1072;
Best Local Similarity 27.4%; Pred. No. 1,5e-64;
Matches 296; Conservative 167; Mismatches 367; Indels 249; Gaps 36;

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QY 299 MHEGAVVVRGSLT-----PLLEGPODGVIT----GDKE 331
DB 435 RHPLVLSLEAASFLYNGFYIPLNLSIFGLSLMAYPKPFALPGJGYPVSESGS 494
QY 332 CVITPSDVV----FDGKSKKNKLNLYRWYLLIGHHEPRLASTKMLERFNNLPKH 367
DB 495 TKLPLSGKKPRLDNPISSTPIST--TFWYIMF-----LVSFTIYVF--SILKIRS 546
QY 388 ENYIPADSEKSEFEVYINLVDOYSENAPTVSRDVEEKPAHAPAPAPVDSMLKMATI 447
DB 547 SEVRPLKSGQNTV--SINKIDTSKRKRKRKRKRVSDE--HSAS----- 587
QY 448 ILSTFLICGVAFITTYPLSMHQQOOLQHQOFKLEKLOLQOQOOLPFHPRGTAOD 507
DB 588 --SNF-----NELESQASEFQNOTDILESENIEI-----QD 617
QY 508 GELDQSGPYSESSGTSPTSPRASNHSLSGSSSASKASSPSLBODDDEFTSVYIG 567
DB 618 ----KSTDPLOKSLDSSLASHLEPAT-----VIOPTDGS-----VTVN 651
QY 568 KISCFKRDVLGHGAEETIYVRCMFNDVAVKRIPECFSEFADREVOLRESDEHPVIR 627
DB 652 SLTVVP--EVIGYSGHGTIYVRYGYEDREVAVKRVLMEFYOLASREITLLQSDNHPVIR 710
QY 628 YFTEKDRPOFYTAIELCAATLOEYVEQK---DPAHLGLEPITLLOQTSSGLAHLHSLNT 684
DB 711 YVCKOKSDFLYIYIELCKCNLSDLIEKPLAYDDELFRKSIDVLSLYOIAVGVSHLSLDL 770
QY 685 VHHDLRPHNLIIMPNAHG----KIKAMISDFGLCKKLANGRHSFGRS--GVPTGEGWIA 739
DB 771 VHHDLRPHNLIIMPNAHG----KIKAMISDFGLCKKLANGRHSFGRS--GVPTGEGWIA 830
QY 740 PEM-----LSECKE-----NPTYVDIFSAGCVYVYVSESHPEGKSLQROAN 784
DB 831 PELTSSLSQSGSEIQVKTREGRIRQASHATDIFALGCIYTYLLTGSMHFGSHYCEGN 890
QY 785 ILGACSLDCLAPKEHEDVYARLEIKMTAMDQKPSANDVUKHPFWSLEKOLQOFOD 844
DB 891 ILGNVCLVHLQSLGEGVLAADLIEDIMIFEPSKRTIEVLNHPFLFMYAKKDLFLID 950
QY 845 VSDRIKESLD--GPIYKOLERGSAVVKMDRENTDPLQDTLRKRTYKGGSVBDLR 902
DB 951 VSDREVEERDPPSLQMLNNSKSVYIGENMTTCILHSSLVDNLGKTRKIDGSKIDILR 1010
QY 903 AMRNKHHYRELPAVYRETLGLTLPDFVCYFYSRPHLAHTYRAM--ELCSHERLFQY 960
DB 1011 VLANKRHHYQDLPESVRYVGLDPLDQFTSYFEVKEKFMILLHCHVAKDVLYESQPKRY 1069

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DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PRO0109; TYRKINASE.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TYRKc; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Serine/threonine-protein kinase; Transferase.
KW SEQUENCE 893 AA; 99087 MW; E32EC6BFC5163255 CRC64;

Query Match 15 0%; Score 770; DB 10; Length 893;
Best Local Similarity 28.6%; Pred. No. 4e-50; Indels 158; Gaps 30;
Matches 234; Conservative 126; Mismatches 300;

QY 242 HINVAETLYETFMGS-----EV-----GRITKKY-----PPPKET--EAKSKLT 281
DB 131 HITSKRPDLNLYYLDGSEHSDILEVHNSGVALLPKLEEFIAETPTIYINDSFYTISKYS 190
QY 282 PTLYGKYSTSLYASPSMHEGAVVVRGSLTLE--GPQIDGVITGDKGECVITPSTD 339
DB 191 TTFVNVADSGEIIYKHSLS--PVALNEVG--PLVEIISKLDAARSGTSANIIVVVRD 245
QY 340 VKFDPGLKSKKNKLNLYR----NYWLLIGHHEPRLASTKMLERFNNLPKHRENVIPAD 394
DB 246 YTSIASDGLHELFNMTRTSTFANYIARYGHQD--MLAQSSCLR--GNIPCTIRTEGPPIK 300
QY 395 SEKSEFEVYINLVDOYSENAPTVSRDVEEKPAHAPAPAP-----VDSK 440
DB 301 -----LYLPDSSDNA--IVLRPVNEVSAVDALERLPKPKLIPQAPGESNVALLDA 349
QY 441 LKDMATITLS-----TFLICGVAFITTYPLSMHQQOOLQHO 477
DB 350 QNOADIALGHFVADTELNTSYTKESYRWLPFTFLMLIMACLVYLAASKYCRQF--- 406
QY 478 QFQKLEKLOLQOQOOLPFHPRGTAODGELDQSGPYSESSGTSPTSPR----- 531
DB 407 -----VIRELK-----PFI-----MRDEKIMD--PRKSGEYTKRRKAKKQDLIN 444
QY 532 ASNHSLSGSSSASKASSPSLEBDDDEFTSVI-----VGKISCFKRDVLGHGAG 583
DB 445 STQIFASDDEGNGTGGSTFAQSNKRAHDSINVELPGLNGRQGLKCYVSKEL--GAGSNG 503
QY 584 TTYVRCMFNDVAVKRIPECFSEFADREVOLRESDEHPNVIYRYCTEKDRQFYTAIE 643
DB 504 TYVEEGSYGGEVAVRRLRSHNDIASKEIENLIASDOPNIYRMVGFEDNDNFYIISLE 563
QY 644 LCAATLOEYVEQK---FAHL-----GL-----EPITLLOQTSSGLAHLHSLNIYH 686
DB 564 KCRCSLADLTQLHVSPPFSNTKGTIDELMRQDLPQAOLIKLMRDVAVAGIVLHSLGITH 623
QY 687 RDLKPHNLIIMPNAHGKIKAMISDFGLCKKLANGRHSFGRSGVPTGEGWIAPEMISLD 746
DB 624 RDLKPHNLIIMPNAHGKIKAMISDFGLCKKLANGRHSFGRSGVPTGEGWIAPEMISLD 746
QY 747 CKENPTYVDIFSAGCVYVYVSESHPEGKSLQROANILGACSLDCLH--PEKIEDVY 804
DB 681 ---RQTRADLFSLGCLIFCITKRGKHPGEYERDMKIIINOFDILFIYDHPE----- 731
QY 805 ARELIEKMTAMDQKPSANDVUKHPFWSLEKOLQOFODVSDRIKESLDGPIYKOLERG 864
DB 732 AYHLISQLDLPDEKRPAYVYVHHPFWSPELCSFLKDTSDRIKTS--ETDILALAG 790
QY 865 GGRAVVKMDRENTDPLQDTLRKRTYKGGSVBDLRANKRHHYRELPAVRETLGT 924
DB 791 INVEARFKWNGEKLDAALLADMGRYKYSPESTRDLRLIRKNSGHYREFSDDLKELLS 850
QY 925 LPDDEVCFYTSRPHLAHTYRAM--ELCSHERLFQY 961
DB 851 LPDGVQYFSSRRPKLLIRYEVMSHCKDEAFSKYF 888

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RESULT 7
Q9FS17 PRELIMINARY; PRT; 893 AA.
Q9FS17: 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE OSIREL.
GN OSIREL.
OS Oryza sativa (Rice).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae;
OC Ehrhartoideae: Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Okushima Y., Koizumi N., Sano H.;
RT Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB031396; BAB20385.1; -
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_kin_actsite.
DR InterPro: IPR001245; Tyr_kin.

RESULT 8
OPFING